ACGCAACTTCGGGCCCAGGGGTCCGCCCCAAGGGGTCCGAAGAGCCTTGAACCGGCCCCGGCTCCTTGACCTTGCTTGT **SEQ ID NO:1**

GGGCCGAAGGACTGCCCCCTGGGCCTGGGTCCGGGTGTGCCCCCTTCTCACTTGAAGACA.GCAGGCCCTGACTCTCCG

CACACTTGGCCCGCCAGCGACGTCACCCAAGCACCTACGAAACTAGTCCCGGGAGCTGGGCAAAGGCACCTACGGGAAG

```
                                        M   A   L   K   F   V   N   K   S   K          10 SEQ ID NO:2
GTTGATCTGGTGGTCTACAAGGGCACAGGCACAAAA ATG GCA CTG AAG TTT GTG AAC AAG AGC AAA          30
                                     ↑SEQ ID NO:3→
 T   K   L   K   N   F   L   R   E   V   S   I   T   N   S   L   S   S   S   P     30
ACC AAG CTG AAG AAC TTC CTA CGG GAG GTG AGC ATC ACC AAC AGC CTC TCC TCC AGC CCC     90

 F   I   I   K   V   F   D   V   V   F   E   T   E   D   C   Y   V   F   A   Q     50
TTC ATC ATC AAG GTC TTT GAC GTG GTC TTT GAG ACA GAG GAC TGC TAC GTC TTT GCC CAG    150

 E   Y   A   P   A   G   D   L   F   D   I   I   P   P   Q   V   G   L   P   E     70
GAG TAC GCA CCT GCT GGG GAC CTG TTT GAC ATC ATC CCT CCC CAG GTG GGG CTC CCT GAG    210

 D   T   V   K   R   C   V   Q   Q   L   G   L   A   L   D   F   M   H   G   R     90
GAC ACG GTG AAG CGC TGT GTG CAG CAG CTG GGC CTG GCG CTG GAC TTC ATG CAC GGG CGG    270

 Q   L   V   H   R   D   I   K   P   E   N   V   L   L   F   D   R   E   C   R    110
CAG CTG GTG CAC CGC GAC ATC AAG CCC GAG AAC GTG CTG CTG TTC GAC CGC GAG TGC CGC    330

 R   V   K   L   A   D   F   G   M   T   R   R   V   G   C   R   V   K   R   V    130
CGC GTA AAG CTG GCC GAC TTC GGC ATG ACG CGC CGC GTG GGC TGC CGC GTC AAG CGC GTG    390

 S   G   T   I   P   Y   T   A   P   E   V   C   Q   A   G   R   A   D   G   L    150
AGC GGC ACC ATC CCT TAC ACG GCG CCT GAG GTG TGC CAG GCG GGC CGC GCC GAC GGG CTG    450

 A   V   D   T   G   V   D   V   W   A   F   G   V   L   I   F   C   V   L   T    170
GCG GTG GAC ACG GGC GTG GAC GTG TGG GCC TTC GGC GTG CTC ATC TTC TGC GTG CTC ACC    510

 G   N   F   P   W   E   A   A   S   G   A   D   A   F   F   E   E   F   V   R    190
GGC AAC TTC CCG TGG GAG GCG GCG TCG GGC GCC GAC GCC TTC TTC GAG GAG TTC GTG CGC    570

 W   Q   R   G   R   L   P   G   L   P   S   Q   W   R   R   F   T   E   P   A    210
TGG CAG CGG GGC CGC CTG CCG GGG CTG CCT TCG CAG TGG CGC CGC TTC ACC GAG CCC GCG    630

 L   R   M   F   Q   R   L   L   A   L   E   P   E   R   R   G   P   A   K   E    230
CTG CGC ATG TTC CAG CGC TTA CTG GCC CTG GAG CCC GAG CGC CGC GGC CCA GCC AAG GAG    690

 V   F   R   F   L   K   H   E   L   T   S   E   L   R   R   R   P   S   H   R    250
GTG TTC CGC TTC CTC AAG CAC GAG CTC ACG TCC GAG CTG CGC CGC CGG CCC TCG CAC CGC    750

 A   R   K   P   P   G   D   R   P   P   A   A   G   P   L   R   L   E   A   P    270
GCG CGC AAG CCC CCC GGG GAC CGC CCG CCC GCC GCC GGG CCA CTG CGC CTC GAG GCG CCT    810

 G   P   L   K   R   T   V   L   T   E   S   G   S   G   S   R   P   A   P   P    290
GGG CCG CTC AAG CGG ACG GTG CTG ACC GAG AGC GGC AGC GGC TCC CGG CCC GCG CCC CCC    870

 A   V   G   S   V   P   L   P   V   P   V   P   V   P   V   P   V   P   V   P    310
GCC GTC GGG TCG GTG CCC TTG CCC GTG CCG GTG CCG GTG CCA GTG CCC GTG CCG GTG CCT    930
```

FIG 1A

```
 V   P   E   P   G   L   A   P   Q   G   P   P   G   R   T   D   G   R   A   D    330
GTG CCC GAG CCC GGC CTA GCT CCC CAG GGG CCC CCC GGC CGG ACC GAC GGC CGC GCG GAC    990

 K   S   K   G   Q   V   V   L   A   T   A   I   E   I   C   V   *                347
AAG AGC AAA GGG CAG GTG GTG CTG GCC ACG GCC ATC GAG ATC TGC GTC TGA              1041
                                                    ←SEQ ID NO:3↑

GTCGCCTCCGCCGCCCTCGGACCCGGGAGCAGCCCGGGCCCGCCCCGAGCCGGTGCCCGGTGCGGCGGTAGGGAATGGA

GCCACCTCGCCGCGGGGCAGGGGGCGCAGCGGTAGACTAGGCAGGACGCGGCCCGGCACCTGGTCCGTCCCCGGCGGGC

TGGTGAGGGGGCCACCAAAGACCCCTAGCGCGGCCTGGTGAGCGGGGGCTTGGCCCAGAGGAGCCAAGCCGCACAGACC

CGAGAATTCGGAGGCCACCACACAACACACACACACACACATACACACACACACACACACGCCAGGAGCAAGGGAGC

TTTCGGGCCACACTCCCAGACGCCTCCCTGAGCCCTGGAACCCGGACTCGTTGCTCCTGGCCTTCCATACCCCCTGGCA

GATCATCCTGCGGTCCCACCCCAGATCCCCTCCTCCTCGCCATCCCATTCTGCCCCCTCCCCACCCTGGGTACAGAAAG

GGACTGAAGTGTTGGGCAGAGAGGGGGCTTAAGGCCCCTGGGCACAGGCTGGGATCAGGGCAGTGAGCGAAGGGCAGCT

GTGTCCTGCCCTTCCTTCTGGAGGCTGGAGGGGAGAGGCCAAGCCCTTGGAAAATGTAGCAAATGTCTGGRWKGTCGCA

TAAGTGCGTGTATGTGCGGGACAGGCCCCGAGAAGCTAGTGACTCCTGCACACCCCCATTGCACAAATGAAATCACAGC

CCAGGAGGGAGGGTAGCTTGGCACTGGCTGAGAAATAGAGCTCTCTCCCCGCCCCTCCCCCTAACCACAAGGGATTGTC

CTGACAACTTGTGGGGATAGAAGGGCTCACAGGGCAGGGGTCTCAGCTGCCCCCATCCTTAGGGCAGGGGAGTTAGTGT

GGAGCCGAGAGCAGGTCCCAGCTCCCCCTGCCAGCCGCACTGTCCCAGGCCCAGGGACCTCTGCCGGGTCCTCCCAGCC

CTTGCCACACAGCCTAGACGTAGTAGCCTGGGCTTCCAGCAGGTGGCGAGCTGGTTCGTGCTGGAAATTTCTCCTGGGT

TTCTTGGGGTCAAACATGCCAACCTCCAAGACCCCATCCTCACGTCTCCCACTTTTCTGGCGCTGGAGTGTGCAGGGCG

TAGGACCTGCATGTGTGGGTGTGAGAATGGGGGCCGGTGGACACCAGGGGGCGAGTGTGTGACTAGGTGTGTGTGCACA

TGTGTAGGGTGCAGACGCATGGGTGCCATCCTTTGCNTTCAATGACTGTGCGTCCAGACCCCAAAAAAGCGGCCCCCCC

ACCACACCCTGNTCCTCCCAGGCAGCTGTCCCAGGGCGCCCAGGCCTGCCTTGCACCACAGCCCTCAGGAAATCCGGCA

AGGAGGCCCCTGCAGGTTGGTTCANGCCCAGGTAGCAAAACAGAGACAACAGCAGCCCCGCCTGACCCCCTGCCCCTNT

CTGTGGAGGCCCGGGACCCCCGCAATAAGCACCACATGGGTGAGGCTGTCCCTGTCAGGGNCCCCTGCCAGGGTCCCTC

CTGGGGTTCTGGGCCATTTGAGGGGCTCTTTGATGGGCCAGGCCNGCCAGAGTGAACTCCGAGCACTTTCTGGCTGGT
```

FIG 1B

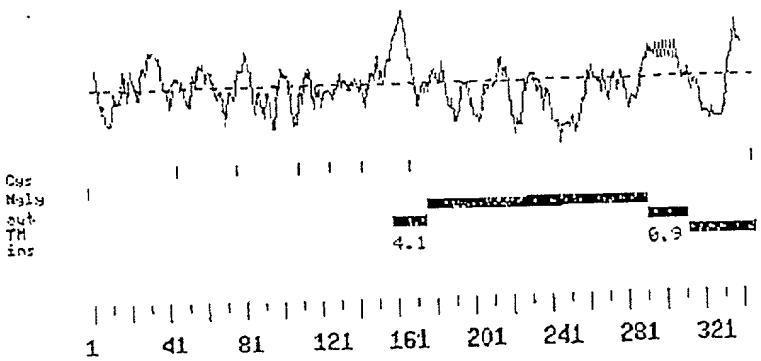

Fig. 2

```
            *->vAvKilkkesls....lrEiqilkrls.HpNIvrllgvfedtddhly  SEQ ID NO:7
               +A+K ++k++++ ++ lrE++i ++ls+ p+I+++++v+ +t+d +
32374     1    MALKFVNKSKTKlknfLREVSITNSLSsSPFIIKVFDVVFETEDCYV 47

            lvmEymegGdLfdylrrngplsekeakkialQilrGleYLHsngivHRDL
            + +Ey++ GdLfd++  +  l+e+ +k+++ Q+  +l+++H++  vHRD+
32374    48 FAQEYAPAGDLFDIIPPQVGLPEDTVKRCVQQLGLALDFMHGRQLVHRDI 97

            KpeNILlden..gtvKiaDFGLArll.eklttfvGTpwYmmAPEvileg.
            KpeN+Ll +++   vK+aDFG+ r ++ + + + GT++Y  APEv  + +
32374    98 KPENVLLFDRecRRVKLADFGMTRRVgCRVKRVSGTIPYT-APEV-CQAg 145

            ....rgysskvDvWSlGviLyElltggplfpgadlpaftggdevdqliif
            + ++   ++ vDvW++Gv+++ +ltg
32374   146 radgLAVDTGVDVWAFGVLIFCVLTG---------------------- 171

            vlklPfsdelpktridpleelfrikkr........rlplpsncSeelkdL
                P++ +      ++ ++ f+   r ++++ ++++ +++++ e+++
32374   172 --NFPWEAA------SGADAFFEEFVRwqrgrlpgLPSQWRRFTEPALRM 213

            lkkcLnkDPskRpGsatakei<-*
              ++L++ P++R     ake+
32374   214 FQRLLALEPERRG---PAKEV    231
```

Fig. 3

```
Query:   226 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDRPPAAGPLRLEAPGPLKRTVLTESGSGS 285
             GPAKEVFRFLKHELTSELRRRPSHRARKPPGDR P  GPLRLEAPGPLKRTVLTESGSGS
Sbjct:     1 GPAKEVFRFLKHELTSELRRRPSHRARKPPGDRLP--GPLRLEAPGPLKRTVLTESGSGS 58  SEQ ID NO:8

Query:   286 R 286
             R
Sbjct:    59 R 59
```

Fig. 4

```
Query:   321 PPGRTDGRADKSKGQVVLATAIEICV 346
             PPGRTDGRADKSKGQVVLATAIEICV
Sbjct:    89 PPGRTDGRADKSKGQVVLATAIEICV 114  SEQ ID NO:9
```

Fig 5

```
Query:   166 FCVLTGNFPWEAASGADAFFEEFVRWQRGRLPGLPSQWRRFTEPALRMFQRLLALEPERR 225
             +C + G FPW+ AS     + E+ +W + + P LP ++  F+E AL++F++ L    + R
Sbjct:     3 YC-MKGKFPWQKASIMCKPYWEWEQWLKRKNPALPKKFNPFSEKALKLFKKSLTPRFKDR 61  SEQ ID NO:10

Query:   226 GPAKEVFRFL-KHELTSELRR 245
               AK++ + L K +L   ++R
Sbjct:    62 WTAKDMRKCLAKEKLLKSVKR 82
```

Fig. 6

```
Query:     4 KFVNKSKTKLKNFLREVSITNSLSSSPFIIKVFDVVFETEDCYVFAQEYAPAGDLFDIIP 63
             K V  SK + +  L E+ +   L ++ F+I +   + +    Y+   +Y+   +  + I
Sbjct:    16 KMVAFSKREEERILLEIDLYKKLENNEFVIDLMAHIVDDITHYLLFDKYSQ--NFLEYIE 73  SEQ ID NO:11

Query:    64 P-QVGLPEDTVKRCVQQLGL--ALDFMHGRQLVHRDIKPENVLLFDRECRRVKLADFG 118
               ++G   D +K      G+  A++ +HG +  H DIKP N+L   +   +K+ DFG
Sbjct:    74 ELKIGGEVDELKHLKYFSGIVSAIEQLHGFEFAHLDIKPANIL---KSGDTIKMIDFG 128
```

Fig. 7

```
Query:    47 VFAQEYAPAGDLFDIIPPQVGLPEDTVKRCVQ---------QLGLALDFMH------GRQ 91
             + A E+ P G L D    +V   +D+ +  +Q          Q+  AL ++H      G++
Sbjct:   175 MIALEWLPGGTLADYFQFKVREKDDSERSPIQLKDMLSILYQVSQALKYIHSQLDEFGQE 234  SEQ ID NO:12

Query:    92 LVHRDIKPENVLLFDRECRR--VKLADFGMTRRVGCRVKRVSGTIPYTAPEV-CQAGRAD 148
             L H  I   NVL+ + + R+  VKL DFG    +G       +  I Y  PE+ C A R
Sbjct:   235 LTHGRIFTRNVLVTEPDLRKCEVKLGDFG-DAPMGLEYS--TPIIAYMPPEILCCAERIP 291

Query:   149 GLAVDTGVDVWAFGVLIF-CVLTGNFP 174
                +   DVW FGV I+ C+  G  P
Sbjct:   292 PHRPEN--DVWMFGVFIWECLTLGAQP 316
```

Fig. 8

```
Query:    77 VQQLGLALDFMHGRQLVHRDIKPENVLL---FDRECRRVKLADFGMTR-----RVGCRVK 128
             + QL  A  ++H  ++  RD+K +N+LL   FD E  ++ +ADFG        +V
Sbjct:   319 IAQLLEACTYLHKHKVAQRDMKSDNILLEYDFDDEIPQLVVADFGCALACDNWQVDYESD 378  SEQ ID NO:13

Query:   129 RVS--GTIPYTAPEVCQAGRADGLAVDTGV-DVWAFGVLIFCVLTGNFPWEAASGADAFF 185
              VS  G     APE+  A     + V+  + D WA G L + VLT + P+
Sbjct:   379 EVSLGGNAKTKAPEIATAVPGKNVKVNFEMADTWAAGGLSYEVLTRSNPFYKLL------ 432

Query:   186 EEFVRWQRGRLPGLPSQ 202
              +   +Q   LP LPS+
Sbjct:   433 -DTATYQESELPALPSR 448
```

Fig. 9

```
Query:    68 LPEDTVKRCVQQLGLALDFMHGRQLVHRDIKPENVLLFDR--ECRRVKLADFGMTRRVGC 125
             LP D ++     L  A+DF+ G  + HRDIKP+N+ +  R    R + L DF +    G
Sbjct:   647 LPVDQLEAYGDYLFGAVDFLEGEGIWHRDIKPDNIAVRIRPNRTRELVLIDFSLA---GY 703  SEQ ID NO:14

Query:   126 RVKRV-SGTIPYTAPEVCQAGRADGLAVDTGVDVWAFGVLIFCVLTGNFP-WEAASGADA 183
               K   +GT  Y  P V    R    + D+  + +A  V +  + +G  P W   S
Sbjct:   704 PAKNTDAGTDGYLDPFVDVITRG---SYDSHAERYAVAVTLHQMASGELPKWGDGSVLPR 760

Query:   184 FFEEFVRWQRGRLPGLPSQWRRFTEPALR-----MFQRLLALEPERRGPAKEVFR--FLK 236
               +    W     P + ++   F +PA+R      FQ+ L  +  +R P  +  R  + K
Sbjct:   761 MTDP-KEWP---YPTIAAE--AF-DPAVRDGLVAFFQKALHRDAGKRFPELKPMRDAWRK 813

Query:   237 HELTSELRRRPSHRARKP-PGD-RPPAAG 263
               L +      SHR R   P D   PA G
Sbjct:   814 VFLDASQTVPSSHRTRPAAPADGAAPAEG 842
```

Fig. 10

```
Query:    30 PFIIKVFDVVFETEDCYVFAQEYAPAGDLFDIIPPQVGLP----EDTVKRCVQQLGLALD 85
             P I+ + +V  E + C++  QE    G +  +     G+P    E+ +   +QQL   LD
Sbjct:    71 PGILAIENVSEEEDRCFLVTQEND--GPILSLTQYLKGIPRKLTEEEIVDIIQQLCSLLD 128
```

SEQ ID NO:15

```
Query:    86 FMHGRQLVHRDIKPENVLL-FDRECRRVKLADFGMTRRVGCR-------------VKRV 130
             ++H   L H      +V + F      + L D G    +  R               ++++
Sbjct:   129 YVHSEGLAHGQWNLHSVHIHFLNGVPNIYLPDLGFASLIRERMFDGFMQDEENRESIEKI 188

Query:   131 SGTIPYTAPEVCQAGRADGLAVDTGVDVWAFGVLIFCVLTGNFPWEAASGADAFFEEFV 189
               + +  PE  Q    +G   DT    +AFG + + +L G FPW         F +F+
Sbjct:   189 RDRLLFHTPEGKQT---NGRETDT----YAFGAITYYLLFGFFPWGIFPKPSKCFPDFI 240
```

Fig. 11

```
Query:    29 SPFIIKVFDVVFETEDC-YVFAQEYAPAGDLFDIIPPQVGLPEDTVKRCVQQLGLALDFM 87
             SP ++ V D++ E E    VF  E      L +++      PE  ++     L   L
Sbjct:    82 SPHVLPVRDLIDEGEWLSLVF--EPRRTITLRELLSAGPVSPE-LLQPLTTALFEGLSAA 138
```

SEQ ID NO:16

```
Query:    88 HGRQLVHRDIKPENVLLFDRECRRVKLADFGMTRRVGCRVKRVSGTIP-YTAPEVCQAGR 146
             H   L+H  I PE V  FD + +R  LA+FG+ RR    ++      P Y APE+   G
Sbjct:   139 HQGALLHTQISPEAVW-FDTQ-KRPLLAEFGLARRTAQELRDHWPHDPRYAAPELLSGG- 195

Query:   147 ADGLAVDTGVDVWAFGVLIFCVLTGNFPWEAASGADAFFEEFVRWQRGRLP----GLPSQ 202
                      D++A    +          EAA+G  A      R Q  RLP    G+P Q
Sbjct:   196 ----PYTPQTDLYALAATLL---------EAATGT-ALSPVSARQQGVRLPSWPAGIPPQ 241

Query:   203 WRRFTEPALRMFQRLLALEPERRGPAKEVFRFLKH-ELTSELRRRPSHRARKPPGDRPPA 261
                  E  L++   + A+       A EV   L+  + T  +  +    A  P    PPA
Sbjct:   242 VAHALESCLQLDPAVRAVS------AAEVLEELRRAQPTQAILSQQEPPAPPPSVPSPPA 295

Query:   262 A 262
             A
Sbjct:   296 A 296
```

Fig. 12

CTTCCTCTTCCTGTGCTCAGTCCCATTAACCTGCCATACCACGGCTCCTCGTCTTCCCAATTCCCTCACCCAGTATTTT SEQID NO:4

CAATCGACCCCCCCCCCGTCCCCCCGCACCTCTTTCTCTCTCGCTATATGTCCTTTCGTGGCCAGTTTGGGCAAGGGGAA

GGACACCACAAGTCGGGGTCTTTCCTCAGCGTTGGGTCGCGGTGGCTGTGAGGGCGGAAGAAAAGGCCAGGCTGAGGGG

AGGGTAGAGGGTGAAAAGCTCGGATCTGTGTTTGGGGAAGGCCAGGCTTGCGCTCCTCGCCGGGTTCCGCGAAGGTTAA

CCTTGGCTGACTTGGCTCGCGAGCAAAGGGCAGCGTCTGAGCTCCCGGCGTTCCAGGAGTGGCCTCTTTTGTAGGAGCA

CCTGAAATGCAGCGTCTGGTGCACTAAGCCGTAGCGGCAGCAGCAGCCACAGCGACAGCGCTGGGGCCCTGTGTAGAAG

CTCCATCCCCCTTGTCTTTGTGCTTGCCTGCGTCCCCAGACTCAGAGATTATCTTAGAAGACCTAGGACTCCAAAA

```
 M   F   P   L   K   D   A   E   M   G   A   F   T   F   F   A   S   A   L   P      20 SEQ ID NO:5
ATG TTT CCC CTG AAG GAC GCT GAA ATG GGA GCC TTT ACC TTC TTT GCC TCG GCT CTG CCA      60
↑SEQ ID NO:6→
 H   D   V   C   G   S   N   G   L   P   L   T   P   N   S   I   K   I   L   G      40
CAT GAT GTT TGT GGA AGC AAT GGA CTT CCT CTC ACA CCA AAT TCC ATC AAA ATT TTA GGG     120

 R   F   Q   I   L   K   T   I   T   H   P   R   L   C   Q   Y   V   D   I   S      60
CGC TTT CAA ATC CTT AAA ACC ATC ACC CAT CCC AGA CTC TGC CAG TAT GTG GAT ATT TCT     180

 R   G   K   H   E   R   L   V   V   V   A   E   H   C   E   R   S   L   E   D      80
AGG GGA AAG CAT GAA CGA CTA GTG GTC GTG GCT GAA CAT TGT GAA CGT AGT CTG GAA GAC     240

 L   L   R   E   R   K   P   V   S   C   S   T   V   L   C   I   A   F   E   V     100
TTG CTT CGA GAA AGG AAA CCT GTG AGC TGT TCA ACG GTT TTG TGT ATA GCA TTT GAG GTT     300

 L   Q   G   L   Q   Y   M   N   K   H   G   I   V   H   R   A   L   S   P   H     120
CTT CAG GGC TTG CAG TAT ATG AAC AAA CAT GGT ATA GTA CAC AGG GCA TTG TCT CCT CAT     360

 N   I   L   L   D   R   K   G   H   I   K   L   A   K   F   G   L   Y   H   M     140
AAT ATC CTG TTG GAC CGA AAG GGA CAT ATT AAA TTG GCT AAA TTT GGA CTT TAT CAC ATG     420

 T   A   H   G   D   D   V   D   F   P   I   G   Y   P   S   Y   L   A   P   E     160
ACA GCT CAT GGT GAT GAT GTT GAT TTC CCA ATA GGG TAT CCC TCG TAC TTG GCC CCT GAG     480

 V   I   A   Q   G   I   F   K   T   T   D   H   M   P   S   K   K   P   L   P     180
GTA ATT GCA CAG GGA ATT TTC AAA ACC ACT GAT CAC ATG CCA AGT AAA AAA CCA TTG CCT     540

 S   G   P   K   S   D   V   W   S   L   G   I   I   L   F   E   L   C   V   G     200
TCT GGC CCC AAA TCA GAT GTA TGG TCT CTT GGA ATC ATT TTA TTT GAG CTT TGT GTG GGA     600

 R   K   L   F   Q   S   L   D   I   S   E   R   L   K   F   L   L   T   L   D     220
AGA AAA TTA TTT CAG AGC TTG GAT ATT TCT GAA AGA CTA AAA TTT TTG CTT ACT TTG GAT     660

 C   V   D   D   T   L   I   V   L   A   E   E   H   G   C   L   D   I   I   K     240
TGT GTA GAT GAC ACT TTA ATA GTT CTG GCT GAA GAG CAT GGT TGT TTG GAC ATT ATA AAG     720

 E   L   P   E   T   V   I   D   L   L   N   K   C   L   T   F   H   P   S   K     260
GAG CTT CCT GAA ACT GTG ATA GAT CTT TTG AAT AAG TGC CTT ACC TTC CAT CCT TCT AAG     780
```

Fig. 13A

R P T P D E L M K D K V F S E V S P L Y 280

AGG CCA ACC CCA GAT GAA TTA ATG AAG GAC AAA GTA TTC AGT GAG GTA TCA CCT TTA TAT 840

T P F T K P A S L F S S S L R C A D L T 300

ACC CCC TTT ACC AAA CCT GCC AGT CTG TTT TCA TCT TCT CTG AGA TGT GCT GAT TTA ACT 900

L P E D I S Q L C K D I N N D Y L A E R 320

CTG CCT GAG GAT ATC AGT CAG TTG TGT AAA GAT ATA AAT AAT GAT TAC CTG GCA GAA AGA 960

S I E E V Y Y L W C L A G G D L E K E L 340

TCT ATT GAA GAA GTG TAT TAC CTT TGG TGT TTG GCT GGA GGT GAC TTG GAG AAA GAG CTT 1020

V N K E I I R S K P P I C T L P N F L F 360

GTC AAC AAG GAA ATC ATT CGA TCC AAA CCA CCT ATC TGC ACA CTC CCC AAT TTT CTC TTT 1080

E D G E S F G Q G R D R S S L L D D T T 380

GAG GAT GGT GAA AGC TTT GGA CAA GGT CGA GAT AGA AGC TCG CTT TTA GAT GAT ACC ACT 1140

V T L S L C Q L R N R L K D V G G E A F 400

GTG ACA TTG TCG TTA TGC CAG CTA AGA AAT AGA TTG AAA GAT GTT GGT GGA GAA GCA TTT 1200

Y P L L E D D Q S N L P H S N S N N E L 420

TAC CCA TTA CTT GAA GAT GAC CAG TCT AAT TTA CCT CAT TCA AAC AGC AAT AAT GAG TTG 1260

S A A A T L P L I I R E K D T E Y Q L N 440

TCT GCA GCT GCC ACG CTC CCT TTA ATC ATC AGA GAG AAG GAT ACA GAG TAC CAA CTA AAT 1320

R I I L F D R L L K A Y P Y K K N Q I W 460

AGA ATT ATT CTC TTC GAC AGG CTG CTA AAG GCT TAT CCA TAT AAA AAA AAC CAA ATC TGG 1380

K E A R V D I P P L M R G L T W A A L L 480

AAA GAA GCA AGA GTT GAC ATT CCT CCT CTT ATG AGA GGT TTA ACC TGG GCT GCT CTT CTG 1440

G V E G A I H A K Y D A I D K D T P I P 500

GGA GTT GAG GGA GCT ATT CAT GCC AAG TAC GAT GCA ATT GAT AAA GAC ACT CCA ATT CCT 1500

T D R Q I E V D I P R C H Q Y D E L L S 520

ACA GAT AGA CAA ATT GAA GTG GAT ATT CCT CGC TGT CAT CAG TAC GAT GAA CTG TTA TCA 1560

S P E G H A K F R R V L K A W V V S H P 540

TCA CCA GAA GGT CAT GCA AAA TTT AGG CGT GTA TTA AAA GCC TGG GTA GTG TCT CAT CCT 1620

D L V Y W Q G L D S L C A P F L Y L N F 560

GAT CTT GTG TAT TGG CAA GGT CTT GAC TCA CTT TGT GCT CCA TTC CTA TAT CTA AAC TTC 1680

N N E A L A Y A C M S A F I P K Y L Y N 580

AAT AAT GAA GCC TTG GCT TAT GCA TGT ATG TCT GCT TTT ATT CCC AAA TAC CTG TAT AAC 1740

F F L K D N S H V I Q E Y L T V F S Q M 600

TTC TTC TTA AAA GAC AAC TCA CAT GTA ATA CAA GAG TAT CTG ACT GTC TTC TCT CAG ATG 1800

I A F H D P E L S N H L N E I G F I P D 620

ATT GCA TTT CAT GAT CCA GAG CTG AGT AAT CAT CTC AAT GAG ATT GGT TTC ATT CCA GAT 1860

L Y A I P W F L T M F T H V F P L H K I 640

CTC TAT GCC ATC CCT TGG TTT CTT ACC ATG TTT ACT CAT GTA TTT CCA CTA CAC AAA ATT 1920

Fig. 13B

F H L W D T L L L G N S S F P F C I G V 660
TTC CAC CTC TGG GAT ACC TTA CTA CTT GGG AAT TCC TCT TTC CCA TTC TGT ATT GGA GTA 1980

A I L Q Q L R D R L L A N G F N E C I L 680
GCA ATT CTT CAG CAG CTG CGG GAC CGG CTT TTG GCT AAT GGC TTT AAT GAG TGT ATT CTT 2040

L F S D L P E I D I E R C V R E S I N L 700
CTC TTC TCC GAT TTA CCA GAA ATT GAC ATT GAA CGC TGT GTG AGA GAA TCT ATC AAC CTG 2100

F C W T P K S A T Y R Q H A Q P P K P S 720
TTT TGT TGG ACT CCT AAA AGT GCT ACT TAC AGA CAG CAT GCT CAA CCT CCA AAG CCA TCT 2160

S D S S G G R S S A P Y F S A E C P D P 740
TCT GAC AGC AGT GGA GGC AGA AGT TCG GCA CCT TAT TTC TCT GCT GAG TGT CCA GAT CCT 2220

P K T D L S R E S I P L N D L K S E V S 760
CCA AAG ACA GAT CTG TCA AGA GAA TCC ATC CCA TTA AAT GAC CTG AAG TCA GAA GTA TCA 2280

P R I S A E D L I D L C E L T V T G H F 780
CCA CGG ATT TCA GCA GAG GAC CTG ATT GAC TTG TGT GAG CTC ACA GTG ACA GGC CAC TTC 2340

K T P S K K T K S S K P K L L V V D I R 800
AAA ACA CCC AGC AAG AAA ACA AAG TCC AGT AAA CCA AAG CTC CTG GTG GTT GAC ATC CGG 2400

N S E D F I R G H I S G S I N I P F S A 820
AAT AGT GAA GAC TTT ATT CGT GGT CAC ATT TCA GGA AGC ATC AAC ATT CCA TTC AGT GCT 2460

A F T A E G E L T Q G P Y T A M L Q N F 840
GCC TTC ACT GCA GAA GGG GAG CTT ACC CAG GGC CCT TAC ACT GCT ATG CTC CAG AAC TTC 2520

K G K V I V I V G H V A K H T A E F A A 860
AAA GGG AAG GTC ATT GTC ATC GTG GGG CAT GTG GCA AAA CAC ACA GCT GAG TTT GCA GCT 2580

H L V K M K Y P R I C I L D G G I N K I 880
CAC CTT GTG AAG ATG AAA TAT CCA AGA ATC TGT ATT CTA GAT GGT GGC ATT AAT AAA ATA 2640

K P T G L L T I P S P Q I * 894
AAG CCA ACA GGC CTC CTC ACC ATC CCA TCT CCT CAA ATA TGA 2682

←SEQ ID NO:6↑

AGAACCAAGAGTGTGACTGCCAAAACTTAGTGTGGCATCAGCACCAACAGCACAGTTCTTCATATCCACGCCACTCTCA

GACAAAACTAGATGTCCAGATTGTTGCATTTCCGTAAAGTTTGTCACGAGACATTTTTTAAAATCTCATAACCCACATG

TTCAGTTATCCATGCAAGAAACTTGACTCTACATGTATTGCTGAAAGAATTTTCTTAACAGTGAAATCTGATCATATAT

TTTTACCACACTGCCACATAAAGCCCAAGAAATTCAGCTGACAAGACAGATTTAGCATTATCAAGAAATC ATTTGCC

CTGAAAAAGCTGTCCTCCATTGTACTGAACAGACAGTCCTGTCGATTGTGTTATTTAGAAACATACACTGAATGTGGGC

TGAAATCATCATCTTTCCATAATGAAAACTGAGAAACTATTCACAATGCATTCCTTATAAATAAATGCTACATTTAGTA

ACTCATTTCACCCAAACAAGAAAGATGTGTGTGTGTGTGTGTATAGGAAGTGGAGTTTATCCCCATTGC AAACT

AATACTTACTCCCAGAAAAATGAAATTTAGAAACCATTTATATTTGATAGAATATTTGGTCAGTTCCTGTAGCAAAGAC

GAATGGCTTAAACAAATTTTCTAGTTTCTTTATCACATGAAAGTCTGTACAGTCAGTCCAGGGCTAGTCTACTGGTTTC

Fig. 13C

CTGATCATTAAGAACTCATTACCTTCTCTCATTGCTTTACAAACCTCAATATGTGGCATCCATCTCATGGATGAAAATG

GCTCCTCAGCTTCTACCATCACATCTGCTATCTAGAAGGAAGAGAATGAGGGAAGGAGGGAGGGGATGAAGAGAAAAGA

AGGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Fig. 13D

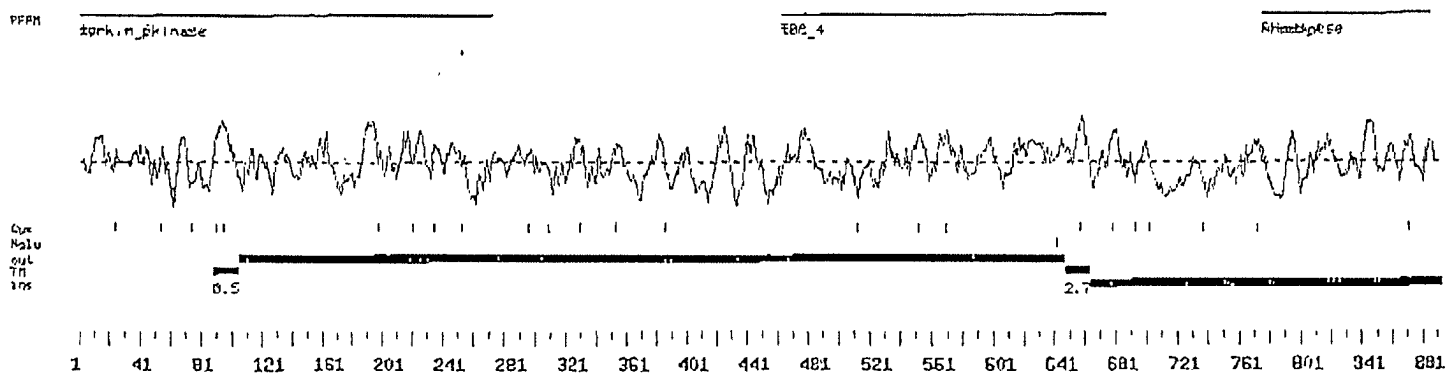

Fig. 14

```
            *->qilkrlsHpNIvrllgvfedtddhlylvmEymegGdLfdylrrngpl  SEQ ID NO:17
               qilk++ Hp ++++ ++ +  +++l +v E++e  +L d+lr+++p
18431    43    QILKTITHPRLCQYVDISRGKHERLVVVAEHCER-SLEDLLRERKPV 88

            sekeakkialQilrGleYLHsngivHRDLKpeNILldengtvKiaDFGLA
            s   +++ia ++l+Gl+Y+  +givHR L p NILld++g++K+a FGL
18431    89 SCSTVLCIAFEVLQGLQYMNKHGIVHRALSPHNILLDRKGHIKLAKFGLY 138

            rll...eklttfvGTpwYmmAPEvi.....leg.rgysskvDv
                ++       G p Y  APEvi ++  +++++ + + + + ++k+Dv
18431   139 HMTahgDDVDFPIGYPSYL-APEVIaqgifkttdhmpSKKpLPSGPKSDV 187

            WSlGviLyElltggplfpgadlpaftggdevdqliifvlklPfsdelpkt
            WSlG+iL+El+ g++lf+++d                    ++    l +
18431   188 WSLGIILFELCVGRKLFQSLD-----------------ISERLKFLLTL 219

            ridpleelfrikkr.rlplpsncSeelkdLlkkcLnkDPskRpGsatake
            ++     ++   +++ l++ ++++e+++dLl+kcL++ PskRp   t  e
18431   220 DCVDDTLIVLAEEHgCLDIIKELPETVIDLLNKCLTFHPSKRP---TPDE 266

            ilnhpwf<-*
            +++++ f
18431   267 LMKDKVF    273
```

Fig. 15

```
            *->vrqgvpsslRgkVWklllgaqelnnclltdnfkgldlfglvpvllla  SEQ ID NO:18
                r  +p  +Rg  W++llg    +
18431   463    ARVDIPPLMRGLTWAALLGVEGAI---------------------- 486

            dkdeYeellnknkektvqdqneKssvgirrldyVEAVEKHPLSDDNDKTK
                Y+++++ ++ +t
18431   487 -HAKYDAIDKDTPIPT--------------------------------- 501

            GSLekgsdekalklredldkIekDlsRTfpdeiffqtrlaeqqlkkdqdl
                          + +Ie D+ R+ + +++
18431   502 -----------------DRQIEVDIPRCHQYDELL--------------- 519

            daydkDEfddeddkneppsikqLrrlLvaYswknpqehlgYvQGMnvils
                          +p+++++ rr+L a ++ +p+  l Y QG   + +
18431   520 --------------SSPEGHAKFRRVLKAWVVSHPD--LVYWQGLDSLCA 553

            pLLlf.lkhgvdldeideeqAFwclvkLmdnylpqkyflndls.glnedl
            p+L++++          +e  A++c ++++ +yl + +fl+d s+ ++e l
18431   554 PFLYLnFN--------NEALAYACMSAFIPKYLYN-FFLKDNShVIQEYL 594

            rvLdslvkeslPeLyshlkkkenktgsgkKknllaldltllifafpwfLt
             v++  + + +PeL++hl+                 + +++++a+pwfLt
18431   595 TVFSQMIAFHDPELSNHLNEI--------------GFIPDLYAIPWFLT 629

            lFarelPleivlrIwDilftyYlgshflifvalAiLkllkskllkh<-*
             F+ ++Pl  ++++wD l++   +s+f++ +++AiL++l++ ll+
18431   630 MFTHVFPLHKIFHLWDTLLLG--NSSFPFCIGVAILQQLRDRLLAN    673
```

Fig. 16

```
Query:   459 IWKEARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDT------PIPTDRQIEVDIPRC 512
             I +E  +D+PP +RG  W  LL V   +    +Y  +D         P P DRQ+EVDIPRC
Sbjct:     1 IQRETNIDVPPTLRGEVWGCLLRVPPSARTRYALLDHAVHHTAAKPTPHDRQLEVDIPRC 60   SEQ ID NO:19

Query:   513 HQYDELLSSPEGHAKFRRVLKAWVVSH--PDLVYWQGLDSLCAPFLYLNFNNEALAYACM 570
             HQY  LL+SP G A+ RR+LKAW + +   P+ VYWQGLDSLCAPFL +N  +EALA+A +
Sbjct:    61 HQYHPLLNSPSGSAQLRRILKAWQIVYLRPEHVYWQGLDSLCAPFLTVNNRDEALAFAQL 120

Query:   571 SAFIPKYLYNFFLKDNSHVIQEYLTVFSQMIAFHDPELSNHLNEIGFIPD 620
             +AF+ +Y++ F+LKDNS VI+EYL  F  + A+HDP L  HL  GF P+
Sbjct:   121 NAFVNRYIHWFYLKDNSEVIKEYLGKFYHLTAYHDPLLYQHLKINGFDPE 170
```

Fig. 17

```
Query:    27 NGLPLTPNSIKILGRFQILKTITHPRLCQYVDISRGKHER--LVVVAEHCERSLEDLLRE 84
             NGLPLTP + ++LGRF  L+ + H  LCQY+   RGKHER   +VV EH   +LED  +
Sbjct:     1 NGLPLTPPAKQMLGRFPYLQELQHDHLCQYLHFIRGKHERDLTIVVMEHYGMNLEDYAKR 60   SEQ ID NO:20

Query:    85 RKPVSCSTVLCIAFEVLQGLQYMNKHGIVHRALSPHNILL----DRKGHIKLAKFGLYHM 140
              P   +       +++  G+ Y+++H IVH  L P++I +    +RK  +KL  +GL+HM
Sbjct:    61 HPPKDEAQNNNFYYQIACGINYLHRHHIVHHNLHPNHIYITDDGNRKLSVKLFNYGLHHM 120

Query:   141 TAHGDDVDFPIGYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXDVWSLGIILFELCVG 200
             T +G    FPIG   Y+APE    I    D++             DVW LG I+ ++ +G
Sbjct:   121 TNYGKYTPFPIGNGRYMAPE----RILNDNDNLFAATYQS-----DVWELGFIMLQIYLG 171

Query:   201 RKL 203
              +L
Sbjct:   172 IEL 174
```

Fig. 18

```
Query:   322 IEEVYYLWCLAGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRXXXXXXXXXXX 381
             + ++Y+LW LAGGD++ EL  + +IRS+ PI  LP  +   G S   GR
Sbjct:   100 LSQIYHLWQLAGGDVQAELKKEGLIRSEAPILGLPQIVRLSGASVCPGRSQAQLMDDRVV 159   SEQ ID NO:21

Query:   382 XXXXCQLRNRLKDVGGEAFYPLLEDDQSNLPHSNSNNELSAAATLPLIIREKDTEYQLNR 441
                 L  RL  +     ++PLL    +  P ++    EL     LPL+IREKD EYQ  R
Sbjct:   160 PLRLKALLQRLSGLPAAVYFPLLHSPR--FP-AHFARELQE---LPLVIREKDIEYQFQR 213

Query:   442 IILFDRLLKAYPYKKNQ 458
             + LF RLL+ YP+   Q
Sbjct:   214 VRLFARLLQGYPHTAEQ 230
```

Fig. 19

```
Query:   207 LDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELPETVIDLLNKCLTFHPSKRPTPDE 266
             L +S  ++ +L        +  L  +A EH C +    ++ + + LL  CL+  P +RP P E
Sbjct:     4 LKLSNVVRKILAFGKSNGALEKIAREHQCHERYVQMDQRLRQLLESCLSVLPKRRPLPGE 63   SEQ ID NO:22

Query:   267 LMKDKVFSEV 276
             L++  +F EV
Sbjct:    64 LLEHPIFEEV 73
```

Fig. 20

```
Query:   636 PLHKIFHLW 644
             PL +I+HLW
Sbjct:    99 PLSQIYHLW 107  SEQ ID NO:23
```

Fig. 21

```
Query:   621 LYAIPWFLTMFTHVFPLHKIFHLWDTLLLGNSSFPFCIGVAILQQLRDRLL-ANGFNECI 679
             LYA  WFLT+F    PL  +  +WD      S   F + +A+L+  ++ LL A+ F E +
Sbjct:     1 LYAFQWFLTLFARELPLETVLRIWDCFFYEGSKILFRVALALLKMHKEELLQADDFEEML 60  SEQ ID NO:24

Query:   680 -LLFSDLP-----EIDIERCVRESINL 700
              L + LP     E D  R + E+ N+
Sbjct:    61 EFLQNMLPKRYRSEEDARRLLEEACNI 87
```

Fig. 22

```
Query:    72 EHCERSLEDLLRERKPVSCSTV---LCIAFEVLQGLQYM----NKHGIVHRALSPHNILL 124
             E  E+  +  + E+K    S V   + IA+++ +GL+Y+    NK  I+HR L P NILL
Sbjct:   136 EMMEKLQKQSMSEKKMEEMSWVSQLMKIAYQIAKGLEYLHSKSNKQNIIHRDLKPENILL 195  SEQ ID NO:25

Query:   125 DR----KGH-----IKLAKFGLYHM 140
             D     KG      +K+A FGL  M
Sbjct:   196 DNNMVAKGDSEIKVVKIADFGLARM 220
```

Fig. 23

```
Query:   152 GYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXDVWSLGIILFELCVGRKLF--QSLDI 209
             G PSY+  + +    +   + +            DVWS G+IL+EL  G+  F   S ++
Sbjct:   245 GTPSYV--KYVGTRWYMAPEVLMGSSYGQYSEKSDVWSFGVILYELLTGKPPFFPGSSEV 302  SEQ ID NO:26

Query:   210 SE-RLKFLLTLDCVDDTLIVLAEEHGCLDIIKE---LP----ETVIDLLNKCLTFHPSKR 261
             ++ ++  ++    V      +  +    + KE    P    E V DL+ KC    P KR
Sbjct:   303 NDSQMNEIMKETMVKSAEYEMPMKMPMPESSKESMSCPSMSSEAVKDLIKKCWQKDPEKR 362

Query:   262 PTPDELMKDKVFSEV 276
             PT  +++++    E+
Sbjct:   363 PTFAQVVEELSAHEI 377
```

Fig. 24

```
Query:   740 PPKT-DLSRESIPLNDLKSEVSPRISAEDLIDLCELTVTGHFXXXXXXXXXXXXXLLVVD 798
             PP+  D+    + L  L+ E  PRISA+D+  L +                    L ++D
Sbjct:    29 PPQALDIGVADVELKHLQQEQCPRISAKDVQFLLD---------------NSPAELALID 73  SEQ ID NO:27

Query:   799 IRNSEDFIRGHISGSINIPFSAAFTAEGELTQGPYTAMLQNFKGKVIVIVGHVAKHTAEF 858
             +R+  +F R H+  SINIPF+     E  L       +    +GK++V V ++ +H+ E
Sbjct:    74 LRSVVEFGRVHVPHSINIPFATVQLGEQRLEALQVPQLEAQLRGKIVVCVSNIHQHSVEV 133

Query:   859 AAHLVKMK 866
               L ++K
Sbjct:   134 GHPLAQLK 141
```

Fig. 25

```
Query:   693 CVRESINLFCWTPKSATYRQHA---QPPKPXXXXXXXXXXAPYFSAECPDPPKTDL---- 745
             CV ES  ++  TPKS T+RQHA   QPP+                  +CP     D+
Sbjct:     3 CVLESQKMYEATPKSITHRQHALRLQPPQALDIGVADVELKHLQQEQCPRISAKDVQFLL 62  SEQ ID NO:28

Query:   746 --SRESIPLNDLKSEVS-PRISAEDLIDLCELTV 776
               S   + L DL+S V   R+     I++   TV
Sbjct:    63 DNSPAELALIDLRSVVEFGRVHVPHSINIPFATV 96
```

Fig. 26

```
Query:   856 AEFAAHLVKMKYPRICILDGGIN---KIKPTGLLT 887
             ++F+  LV     R CIL  G N    I+P  L++
Sbjct:   152 SQFSHFLVACGVQRTCILHKGFNVLHSIEPNILIS 186  SEQ ID NO:29
```

Fig. 27

```
Query:   506 EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPD--LVYWQGLDSLCAPFLYLNFNNE 563
             + DI  C +Y+     P  + + +  L+ + V +P   ++ + G     APF YL
Sbjct:   336 DTDIGGCFEYNTF-PPPGKYYRGKLGLEEYAVFYPPNGVIPFHGFCMYAAPFCYLYHEPS 394  SEQ ID NO:30

Query:   564 ALAYACMSAFIPKYLYNFFLKDNSHV--IQEYLTVFSQMIAFHDPELSNHLNEIGFIPDL 621
              L Y     +I +Y +      N+H   I     +F +++  ++P+L  H  EIG  P
Sbjct:   395 KLYYTFREFYI-RYCHRLHTI-NTHPQGIVSLCLLFEKLLQTYEPQLWYHFREIGAQPLR 452

Query:   622 YAIPWFLTMFTHVFPLHKIFHLWDTLLLGNS 652
              +  W +  F+   P  ++  LWD +L  NS
Sbjct:   453 ISFKWMMRAFSGHLPPDQLLLLWDRILGYNS 483
```

Fig. 28

```
Query:    77 SLEDLLRERKPVSCSTVLC--IAFEVLQGLQYMNKHGIVHRALSPHNILLDRKGHIKLAK 134
             S   LLR   P   S  L   I F  ++GL Y++++G +HR++   +IL+   G + L+
Sbjct:     5 SASQLLRTYFPEGMSETLIRNILFGAVRGLNYLHQNGCIHRSIKASHILISGDGLVTLSG 64  SEQ ID NO:31

Query:   135 FG-LYHMTAHGDD----VDFP---IGYPSYLAPEVIAQGIFKTTDHMXXXXXXXXXXXXD 186
               L+ +  HG       DFP        +L+PE++ Q +     H             D
Sbjct:    65 LSHLHSLVKHGQRHRAVYDFPQFSTSVQPWLSPELLRQDL-----H-------GYNVKSD 112

Query:   187 VWSLGIILFELCVGRKLFQSLDISERL 213
             ++S+GI   EL  G+  FQ +  ++ L
Sbjct:   113 IYSVGITACELASGQVPFQDMHRTQML 139
```

Fig. 29

```
Query:   240 KELPETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEV 276
             K        L+  CL   P KRP+   L+    F ++
Sbjct:   198 KTFSPAFFSLVQLCLQQDPEKRPSASSLLSHVFFKQM 234  SEQ ID NO:32
```

Fig. 30

```
Query:   596 VFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPLHKIFHLWDTLLLGNSSFP 655
             +F  ++ +HDPEL NHL+      PD+Y + WF ++F             LWD  +     F
Sbjct:    18 LFRLLLQYHDPELCNHLDTKKCTPDMYTLNWFGSLFASCCSTEVCHALWDLYIQQADPFM 77   SEQ ID NO:33

Query:   656 -FCIGVAILQQLRDRLL---ANGFNECILLFSDLP-EIDIE 691
              F + + IL    ++ +L    ++     E I     ++P +++IE
Sbjct:    78 VFFLALIIILINAKEEILQMKSDSKEEVIKFLENMPCQLNIE 118
```

Fig. 31

```
Query:   796 VVDIRNSEDFIRGHISGSINI 816
             +VD R +E +   GH+S + ++
Sbjct:   194 IVDCRPAEQYNAGHLSTAFHL 214   SEQ ID NO:34
```

Fig. 32

```
Query:   112 IVHRALSPHNILLDRKGHIKLAKFGLYHMTAHGDDVD--FPIGYP--SYLAPEVIAQGIF 167
             ++HR + P +IL+ ++G  KLA F          + +D +  FP  Y     + P  +    +
Sbjct:     1 VIHRNICPESILITKRGSWKLAGFDFCVSAQNPNDQENYFPCHYEWDPRIPPLPLQPNLD 60   SEQ ID NO:35

Query:   168 KTTDHMXXXXXXXXXXXXDVWSLGIILFELCVGRKLFQSLDISERLKFLLTLDCVDDTLI 227
                               D++SLG +++ +   G K      +D +     ++        +    +TL
Sbjct:    61 YLAPEYVTSSTCTVGSASDMFSLGCLIYAIYNGGKPL--IDANNNDEYKSNYNKYMNTLN 118

Query:   228 VLAEEHGCLDIIKELPETVIDLLNKCLTFHPSKRPTPDELMKDKVF 273
               L    H  ++ +     PE  + L  + L+   P+ RPT   EL     K F
Sbjct:   119 SLT--HESMNNLP--PENLKESLKRMLSMDPTVRPTAQELTLIKYF 160
```

Fig. 33

```
Query:   744 DLSRESIPLNDLKSEVSPRI--SAEDL-IDLCE 773
             DL   +   P   D+KS + P +   + ED   I +C+
Sbjct:   273 DLLLQKTPPEDIKSNILPMLYYAFEDSDIQICQ 305   SEQ ID NO:36
```

Fig. 34